

# ESP 121: Lab 5

## Stochasticity

Open `SIRrand.R`. This runs the SIR model with births and deaths:

$$\begin{aligned}\frac{dS}{d\tau} &= \rho(N - S) - R_0 S \frac{I}{N} \\ \frac{dI}{d\tau} &= R_0 S \frac{I}{N} - (1 - \rho)I - \rho I \\ \frac{dR}{d\tau} &= (1 - \rho)I - \rho R\end{aligned}$$

both in the deterministic case and with demographic stochasticity. Here  $R_0 = \frac{\beta}{\gamma + \mu}$ ,  $\rho = \frac{\mu}{\gamma + \mu}$ , and  $\tau = (\gamma + \mu)t$ . Note that time and the parameters are non-dimensionalized but the population sizes of susceptibles  $S$ , infecteds  $I$ , and recovered  $R$  are not. Expressing these state variables in terms of individuals (rather than the dimensionless proportion of the total population) is necessary to follow individual-by-individual variation in the implementation with demographic stochasticity.

Given demographic stochasticity, individuals are counted as individuals, where you can only have whole numbers of individuals (i.e., the number of susceptibles is always a whole number such as 500, never with a fraction of an individual such as 500.3, as can happen in the deterministic case). Each individual undergoes an event (birth, death, infection, recovery) with a probability determined by the rates for these processes. To implement demographic stochasticity for a continuous-time model, we first calculate the wait time until the next event (change in class of one individual through a birth, death, infection, or recovery) by drawing a random number from an exponential distribution based on the sum of the rates for all events. We then calculate which event occurred by the drawing a second random number, with the probability of each event given by its relative rate. The event table is:

Event	Scaled rate	Outcome		
Birth	$\rho N$	$S \rightarrow S + 1$	$I \rightarrow I$	$R \rightarrow R$
Death of a susceptible	$\rho S$	$S \rightarrow S - 1$	$I \rightarrow I$	$R \rightarrow R$
Infection	$R_0 SI/N$	$S \rightarrow S - 1$	$I \rightarrow I + 1$	$R \rightarrow R$
Death of an infected	$\rho I$	$S \rightarrow S$	$I \rightarrow I - 1$	$R \rightarrow R$
Recovery of an infected	$(1 - \rho)I$	$S \rightarrow S$	$I \rightarrow I - 1$	$R \rightarrow R + 1$
Death of a recovered	$\rho R$	$S \rightarrow S$	$I \rightarrow I$	$R \rightarrow R - 1$

Run the model with different values of total population size  $N$ , infection rate  $R_0$ , and birth/death rate  $\rho$ . Run it a few times in each case, as the outcome of the stochastic simulation can vary with each run. It may take a moment to do a given run.

1. Deterministic vs. stochastic runs: how does incorporating demographic stochasticity affect the dynamics?
2. Runs with different parameter values: for the model with demographic stochasticity, how does changing each of  $N$ ,  $R_0$ , and  $\rho$  change the cycles (e.g., are they dampened or amplified, and at higher or lower frequency, with increasing or decreasing values of each parameter)? Why? (Be sure to explore several values in each case.)